



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 144217

TO: Nita M Minnifield  
Location: rem/3c01/3c18  
Art Unit: 1645  
Tuesday, February 22, 2005  
Case Serial Number: 10/680349

From: Paul Schulwitz  
Location: Biotech-Chem Library  
REM-1A65  
Phone: (571)272-2527

[paul.schulwitz@uspto.gov](mailto:paul.schulwitz@uspto.gov)

### Search Notes

Examiner Minnifield,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz  
Technical Information Specialist  
STIC Biotech/Chem Library  
(571)272-2527

STIC-Biotech/ChemLib

144217

my

From: Minnifield, Nita  
Sent: Thursday, February 03, 2005 11:04 PM  
To: STIC-Biotech/ChemLib  
Subject: sequence search

10/680349

STIC

Please do a commercial and interference sequence search on SEQ ID NO: 41 (nt) and SEQ ID NO: 42 (aa) of this application.

Please provide a paper copy of the results.

Thanks,  
Minnifield,

~~71796~~

Art Unit 1645  
Office REM-3C01  
Mailbox REM-3C18  
571-272-0860

RECEIVED  
FEB -4 2005  
STIC-Biotech/ChemLib  
(STIC)

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STAFF USE ONLY

Searcher: \_\_\_\_\_  
Searcher Phone: 2- \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date Completed: 2/2 \_\_\_\_\_  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

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Type of Search

NA Sequence: # \_\_\_\_\_  
AA Sequence: # \_\_\_\_\_  
Structure: # \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

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Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other(Specify): \_\_\_\_\_

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GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: February 17, 2005, 16:44:35 / Search time 166 Seconds  
(without alignments)  
652.367 Million cell updates/sec

Title: US-10-680-349-42

Perfect score: 1462  
Sequence: 1 MWYKILVRSALISILP.....ASVTLDVGFGEIGMRETF 280

Scoring table: BLOSUM62

Gapop 10.0 ; Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: GeneSeqP1980s:\*  
2: GeneSeqP1990s:\*  
3: GeneSeqP2000s:\*  
4: GeneSeqP2001s:\*  
5: GeneSeqP2002s:\*  
6: GeneSeqP2003s:\*  
7: GeneSeqP2003bs:\*  
8: GeneSeqP2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1462	100.0	280	AAU96116	Aau96116 Ehrlichia
2	1462	100.0	280	ABG77938	Abg77938 Ehrlichia
3	1462	100.0	280	ADA09741	Ada09741 E. chaffe
4	1202.5	82.3	283	AAU06944	Aau06944 E. chaffe
5	1202.5	82.3	283	AAU96106	Aau96106 Ehrlichia
6	1202.5	82.3	283	AAU73413	Aau73413 Ehrlichia
7	1202.5	82.3	283	ABG77936	Abg77936 Ehrlichia
8	1202.5	82.3	283	ADA09737	Ada09737 E. chaffe
9	715	48.9	165	AAU06970	Aau06970 E. canis
10	644.5	44.1	281	AAU06943	Aau06943 E. chaffe
11	644.5	44.1	281	AAU96105	Aau96105 Ehrlichia
12	644.5	44.1	281	AAU73418	Aau73418 Ehrlichia
13	644.5	44.1	281	ABG77935	Abg77935 Ehrlichia
14	644.5	44.1	281	ADA09735	Ada09735 E. chaffe
15	629.5	43.1	276	AAU51095	Aau51095 Ehrlichia
16	629.5	43.1	276	AAU36189	Aau36189 Ehrlichia
17	629.5	43.1	276	AAU04199	Aau04199 Variable
18	622	42.5	286	AAU51092	Aau51092 Ehrlichia
19	622	42.5	286	AAU06959	Aau06959 E. canis
20	621	42.5	288	ABG77950	Abg77950 Ehrlichia
21	621	42.5	288	ADA09765	Ada09765 E. canis
22	620	42.4	286	AAU06946	Aau06946 E. chaffe
23	620	42.4	286	AAU36186	Aau36186 Ehrlichia
24	620	42.4	286	AAU04196	Aau04196 Variable
25	620	42.4	286	AAU96108	Aau96108 Ehrlichia

26	620	42.4	286	AAU73415	Aau73415 Ehrlichia
27	620	42.4	286	ABG77938	Abg77938 Ehrlichia
28	620	42.4	286	ADA09741	Ada09741 E. chaffe
29	606	41.5	280	ABG77953	Abg77953 Ehrlichia
30	605	41.4	280	AAU06948	Aau06948 E. chaffe
31	605	41.4	280	AAU96110	Aau96110 Ehrlichia
32	605	41.4	280	ABG77940	Abg77940 Ehrlichia
33	605	41.4	280	ADA09745	Ada09745 E. chaffe
34	603	41.2	280	AAU51094	Aau51094 Ehrlichia
35	603	41.2	280	AAU36188	Aau36188 Ehrlichia
36	603	41.2	280	AAU04198	Aau04198 Variable
37	603	41.2	280	AAU73417	Aau73417 Ehrlichia
38	601	41.1	280	AAU06962	Aau06962 E. canis
39	601	41.1	280	AAU71479	Aau71479 Ehrlichia
40	601	41.1	280	AAU96102	Aau96102 Ehrlichia
41	601	41.1	280	AAU09771	Aau09771 E. canis
42	592	40.5	285	AAU06957	Aau06957 E. chaffe
43	592	40.5	285	AAU73408	Aau73408 Ehrlichia
44	592	40.5	285	ABG77949	Abg77949 Ehrlichia
45	588	40.2	278	AAU71477	Aau71477 Ehrlichia

## ALIGNMENTS

1-3

RESULT 1  
AAU96116  
ID AAU96116 standard; protein; 280 AA.

XX AAU96116;

DT 02-JUL-2002 (first entry)

DE Ehrlichia canis p28-2.

KW Ehrlichia canis infection; vaccine; serodiagnostic; p28; antibacterial.

OS Ehrlichia canis.

PN W0200222782-A2.

PD 21-MAR-2002.

PF 12-SEP-2001; 2001WO-US028759.

PR 12-SEP-2000; 2000US-00660587.

PA (RESE-) RES DEV FOUND.

XX Walker DH, Yu X, McBride JW;

PI WPI; 2002-351882/38.

DR N-PSDB; ABK68876.

PT New recombinant homologous 28 kilodalton immunodominant protein from

XX Ehrlichia canis, useful for treating Ehrlichia canis infections.

PS Claim 16; Fig 14; 106pp; English.

XX The invention relates to a recombinant homologous 28 kDa immunodominant

CC protein, p28, (I), of Ehrlichia canis. (I), a 28-kDa antigen preferably

CC dispersed in a pharmaceutically acceptable carrier, is useful for

CC inhibiting E. canis infection in a subject. (I) is useful in the

CC development of vaccines and serodiagnostic that are particularly

CC effective for disease prevention and serodiagnosis. AAU96100-AAU96118

XX represent the 28-kDa antigen amino acid sequences of the invention

SQ Sequence 280 AA;

Query Match 100.0%; Score 1462; DB 5; Length 280;

Best Local Similarity 100.0%; Pred. No. 1.9e-138; Indels 0; Gaps 0;

Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OM protein - protein search, using sw model

Run on: February 17, 2005, 16:49:10 ; Search time 43 Seconds

(without alignments)  
486.087 Million cell updates/sec

Title: US-10-680-349-42

Perfect score: 1462

Sequence: 1 MNXKILVRSLALISLMSILP.....ASVTLDVGVFGSGIGMRFTF 280

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Issued Patents AA\*  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1462	100.0	280	3	US-09-660-587-42
2	1462	100.0	280	4	US-09-314-701-46
3	1462	100.0	280	4	US-09-811-007A-42
4	1202.5	82.3	283	3	US-09-660-587-10
5	1202.5	82.3	283	4	US-09-261-358A-10
6	1202.5	82.3	283	4	US-09-201-458-6
7	1202.5	82.3	283	4	US-09-314-701-4
8	1202.5	82.3	283	4	US-09-811-007A-10
9	644.5	44.1	281	3	US-09-660-587-9
10	644.5	44.1	281	4	US-09-261-358A-9
11	644.5	44.1	281	4	US-09-201-458-5
12	644.5	44.1	281	4	US-09-811-007A-9
13	644.5	43.9	281	4	US-09-314-701-2
14	629.5	43.1	276	3	US-08-953-326-18
15	629.5	43.1	276	4	US-09-553-662-18
16	629.5	43.1	276	4	US-10-062-994-18
17	621	42.5	288	4	US-09-314-701-32
18	620	42.4	286	3	US-08-953-326-15
19	620	42.4	286	3	US-09-660-587-12
20	620	42.4	286	4	US-09-261-358A-12
21	620	42.4	286	4	US-09-201-458-8
22	620	42.4	286	4	US-09-314-701-8
23	620	42.4	286	4	US-09-553-662-15
24	620	42.4	286	4	US-10-062-994-15
25	620	42.4	286	4	US-09-811-007A-12
26	605	41.4	280	3	US-09-660-587-14
27	605	41.4	280	4	US-09-261-358A-14

28	605	41.4	280	4	US-09-201-458-10	Sequence 10, Appl
29	605	41.4	280	4	US-09-314-701-12	Sequence 12, Appl
30	605	41.4	280	4	US-09-811-007A-14	Sequence 14, Appl
31	603	41.2	280	3	US-08-953-326-17	Sequence 17, Appl
32	603	41.2	280	4	US-09-553-662-17	Sequence 17, Appl
33	603	41.2	280	4	US-10-062-994-17	Sequence 17, Appl
34	601	41.1	280	3	US-09-660-587-6	Sequence 6, Appl
35	601	41.1	280	4	US-09-261-358A-6	Sequence 6, Appl
36	601	41.1	280	4	US-09-314-701-38	Sequence 38, Appl
37	601	41.1	280	4	US-09-811-007A-6	Sequence 6, Appl
38	588	40.2	278	4	US-09-660-587-2	Sequence 2, Appl
39	588	40.2	278	4	US-09-261-358A-2	Sequence 2, Appl
40	588	40.2	278	4	US-09-201-458-2	Sequence 2, Appl
41	588	40.2	278	4	US-09-811-007A-2	Sequence 2, Appl
42	588	40.2	307	4	US-09-314-701-36	Sequence 36, Appl
43	587	40.2	285	4	US-09-314-701-30	Sequence 30, Appl
44	583	39.9	278	3	US-08-953-326-16	Sequence 16, Appl
45	583	39.9	278	3	US-09-660-587-13	Sequence 13, Appl

## ALIGNMENTS

RESULT 1	US-09-660-587-42	Application US/09660587
Sequence 42, Appl	Patent No. 6392023	
GENERAL INFORMATION:		
APPLICANT:	Walker, David H.	
APPLICANT:	McBride, Jere W.	
APPLICANT:	Yu, Xue-Jie	
TITLE OF INVENTION:	Homologous 28-kilodalton Immunodominant Protein	
TITLE OF INVENTION:	Genes of Ehrlichia canis and Uses Thereof	
FILE REFERENCE:	D6152CIP2	
CURRENT APPLICATION NUMBER:	US/09/660,587	
CURRENT FILING DATE:	2000-09-12	
PRIOR APPLICATION NUMBER:	09/261,358	
PRIOR FILING DATE:	1999-03-03	
NUMBER OF SEQ ID NOS:	46	
SEQ ID NO 42		
LENGTH:	280	
TYPE:	PRT	
ORGANISM:	Ehrlichia canis	
FEATURES:		
OTHER INFORMATION:	amino acid sequence of E. canis p28-2 protein	
US-09-660-587-42		
Query Match	100.0%; Score 1462; DB 3; Length 280;	
Best Local Similarity	100.0%; Pred. No. 8.2e-151;	
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 MNXKILVRSLALISLMSILPYOSPADPVGSRITDNKSGFISAKYNSISHPRKSAET 60	
DB	1 MNXKILVRSLALISLMSILPYOSPADPVGSRITDNKSGFISAKYNSISHPRKSAET 60	
QY	61 PINGNSLTKKVFGLKKDGDITKDDFTFVAAGIDFONNLISGSGSIGSMQPRIELE 120	
DB	61 PINGNSLTKKVFGLKKDGDITKDDFTFVAAGIDFONNLISGSGSIGSMQPRIELE 120	
QY	121 AAQOFPKNTDNDNDNGEYHGFALSRDAMEDQYVVKDGTIFMSLMVNTCYDIT 180	
DB	121 AAQOFPKNTDNDNDNGEYHGFALSRDAMEDQYVVKDGTIFMSLMVNTCYDIT 180	
QY	181 AEGSFPVACAGIGADLITFMDLNKFAVQKIGISYPIETBVSFISGYHGVGNK 240	
DB	181 AEGSFPVACAGIGADLITFMDLNKFAVQKIGISYPIETBVSFISGYHGVGNK 240	
QY	241 FEKIPVITPVVNDAPQTSASVTLGVFGSGIGMRFTF 280	
DB	241 FEKIPVITPVVNDAPQTSASVTLGVFGSGIGMRFTF 280	
RESULT 2		

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OM protein - protein search, using sw model

Run on: February 17, 2005, 16:57:26 / Search time 133 Seconds

(without alignments)  
688.929 Million cell updates/sec

Title: US-10-680-349-42

Perfect score: 1462

Sequence: 1 MYKKILVRSALISLMSILP.....ASVTLVGVFGGIGMRFPT 280

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Total number of hits satisfying chosen parameters: 1380268

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
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- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
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- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1462	100.0	280	10	US-09-811-007-42
2	1462	100.0	280	13	US-10-062-624-42
3	1462	100.0	280	13	US-10-059-964-48
4	1462	100.0	280	14	US-10-062-051-42
5	1462	100.0	280	14	US-10-062-920-42
6	1462	100.0	280	14	US-10-314-639-48
7	1462	100.0	280	16	US-10-680-349-42
8	1262.5	82.3	283	9	US-09-846-808-14
9	1202.5	82.3	283	10	US-09-811-007-10
10	1202.5	82.3	283	13	US-10-062-624-10
11	1202.5	82.3	283	13	US-10-059-964-4
12	1202.5	82.3	283	14	US-10-062-051-10
13	1202.5	82.3	283	14	US-10-284-986-14

14	1202.5	82.3	283	14	US-10-062-920-10	Sequence 10, Appl
15	1202.5	82.3	283	14	US-10-314-639-4	Sequence 4, Appl
16	1202.5	82.3	283	14	US-10-369-293-14	Sequence 14, Appl
17	1202.5	82.3	283	14	US-10-285-042-14	Sequence 14, Appl
18	1202.5	82.3	283	16	US-10-680-349-10	Sequence 19, Appl
19	644.5	44.1	281	9	US-09-846-808-19	Sequence 9, Appl
20	644.5	44.1	281	10	US-09-811-007-9	Sequence 9, Appl
21	644.5	44.1	281	13	US-10-062-624-9	Sequence 9, Appl
22	644.5	44.1	281	14	US-10-062-051-9	Sequence 9, Appl
23	644.5	44.1	281	14	US-10-284-986-19	Sequence 9, Appl
24	644.5	44.1	281	14	US-10-062-920-9	Sequence 9, Appl
25	644.5	44.1	281	14	US-10-369-293-19	Sequence 9, Appl
26	644.5	44.1	281	14	US-10-285-042-19	Sequence 9, Appl
27	644.5	44.1	281	16	US-10-680-349-9	Sequence 9, Appl
28	642.5	43.9	281	13	US-10-059-964-2	Sequence 2, Appl
29	642.5	43.9	281	14	US-10-314-639-2	Sequence 2, Appl
30	629.5	43.1	276	13	US-10-062-994-18	Sequence 18, Appl
31	629.5	43.1	276	13	US-10-062-994-18	Sequence 18, Appl
32	629.5	43.1	276	16	US-10-722-077-18	Sequence 18, Appl
33	621	42.5	288	13	US-10-059-964-32	Sequence 32, Appl
34	621	42.5	288	14	US-10-314-639-32	Sequence 32, Appl
35	620	42.4	286	9	US-09-846-808-16	Sequence 16, Appl
36	620	42.4	286	10	US-09-811-007-12	Sequence 12, Appl
37	620	42.4	286	13	US-10-062-994-15	Sequence 15, Appl
38	620	42.4	286	13	US-10-062-624-12	Sequence 12, Appl
39	620	42.4	286	13	US-10-059-964-8	Sequence 8, Appl
40	620	42.4	286	13	US-10-062-994-15	Sequence 15, Appl
41	620	42.4	286	14	US-10-062-051-12	Sequence 12, Appl
42	620	42.4	286	14	US-10-284-986-16	Sequence 16, Appl
43	620	42.4	286	14	US-10-062-920-12	Sequence 12, Appl
44	620	42.4	286	14	US-10-314-639-9	Sequence 9, Appl
45	620	42.4	286	14	US-10-369-293-16	Sequence 16, Appl

## ALIGNMENTS

RESULT 1  
US-09-811-007-42  
Sequence 42, Application US/09811007  
Publication No. US20030185849A1  
GENERAL INFORMATION:  
APPLICANT: Walker, David H.  
APPLICANT: McBride, Jere W.  
APPLICANT: Yu, Xue-Jie  
TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein  
FILE REFERENCE: D6152CIP2  
CURRENT APPLICATION NUMBER: US/09/811,007  
CURRENT FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 09/660,587  
NUMBER OF SEQ ID NOS: 46  
SEQ ID NO 42  
LENGTH: 280  
TYPE: PRT  
ORGANISM: Ehrlichia canis  
FEATURE:  
OTHER INFORMATION: amino acid sequence of E. canis p28-2 protein  
US-09-811-007-42

Query Match 100.0%: Score 1462; DB 10; Length 280;  
Best Local Similarity 100.0%: Pred. No. 7, 3e-136;  
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYKKILVRSALISLMSILPYOSFADPVGSRITNDKEGFYSKYNPSISHPKFSAEET 60  
DB 1 MYKKILVRSALISLMSILPYOSFADPVGSRITNDKEGFYSKYNPSISHPKFSAEET 60

QY 61 PINGTSLTKVVGKLGKDDITKDDFTVAPRIDPQNNLISGFSGISGMDGPRILER 120  
DB 61 PINGTSLTKVVGKLGKDDITKDDFTVAPRIDPQNNLISGFSGISGMDGPRILER 120

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OM protein - protein search, using sw model

Run on: February 17, 2005, 16:47:35 ; Search time 178 Seconds

(without alignments)  
805,518 Million cell updates/sec

Title: US-10-680-349-42

Perfect score: 1462  
Sequence: 1 NMYKKILVRSALISIMSLIP.....ASVTLDVGFGGEGNRFPT 280

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database: UniProt\_03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1462	100.0	280	2	Q9F476
2	1452	99.3	280	2	Q84HU1
3	1224.5	83.8	283	2	Q8G8D6
4	1217.5	83.3	283	2	Q8G8I2
5	1217.5	83.3	283	2	Q8G8U4
6	1202.5	82.3	283	2	Q8G8U4
7	1124	76.9	282	2	Q9R443
8	1120	76.6	282	2	Q9RW41
9	983	67.2	250	2	Q8VTT7
10	665.5	45.5	275	2	Q93DD4
11	655	44.8	276	2	Q8GCU0
12	651	44.5	276	2	Q8G8I7
13	648	44.3	280	2	Q9ZG09
14	647	44.3	276	2	Q93DD1
15	645.5	44.2	281	2	Q93DD2
16	644.5	44.1	281	2	Q9ACV9
17	644	44.0	280	2	Q8S816
18	628	43.0	280	2	Q93DD3
19	621	42.5	288	2	Q9ZG02
20	620	42.4	286	2	Q52105
21	605	41.4	280	2	Q52107
22	605	41.4	291	2	Q8G8P3
23	601	41.1	280	2	Q9ADV3
24	600	41.0	280	2	Q9F473
25	599	41.0	281	2	Q8G921
26	598	40.9	291	2	Q8G8G2
27	592	40.5	285	2	Q9L6V5
28	589	40.3	287	2	Q8GCU3
29	588	40.2	278	2	Q9R3J3
30	588	40.2	278	2	Q9R8A5
31	588	40.2	278	2	Q9R8A6

32	588	40.2	278	2	Q9R8A7	Q9-8a7 ehrlichia c
33	588	40.2	278	2	Q9R8A8	Q9-8a8 ehrlichia c
34	588	40.2	278	2	Q9R8A9	Q9-8a9 ehrlichia c
35	588	40.2	307	2	Q9ZGJ1	Q9ZGJ1 ehrlichia c
36	583.5	39.9	277	2	Q8G8W7	Q8G8W7 ehrlichia c
37	583.5	39.9	277	2	Q8G8W7	Q8G8W7 ehrlichia c
38	583	39.9	278	2	Q52106	Q52106 ehrlichia c
39	583	39.9	278	2	Q9F472	Q9F472 ehrlichia c
40	573.5	39.2	279	2	Q8G8Q1	Q8G8Q1 ehrlichia c
41	573	39.2	278	2	Q8G8O5	Q8G8O5 ehrlichia c
42	569	38.9	280	2	Q8G8J3	Q8G8J3 ehrlichia c
43	567.5	38.8	281	2	Q9G6H1	Q9G6H1 cowdria rum
44	567	38.8	290	2	Q46333	Q46333 cowdria rum
45	566.5	38.7	271	2	Q69197	Q69197 ehrlichia c

#### ALIGNMENTS

RESULT 1	Q9F476	PRELIMINARY;	PRT;	280 AA.
ID	Q9F476			
AC	Q9F476;			
DT	01-MAR-2001 (TREMBLrel. 16, Created)			
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DE	05-VUL-2004 (TREMBLrel. 27, Last annotation update)			
DE	P28-2 (Major outer membrane protein P30-10).			
GN	Name=p28-2; Synonyms=p30-10;			
OS	Ehrlichia canis.			
OC	Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;			
OC	Anaplasmataceae; Ehrlichia.			
OX	NCBI_TaxID=944;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Jake;			
RX	MEDLINE=99242757; PubMed=10225842;			
RA	McBride J.W., Yu X.J., Walker D.H.;			
RT	Molecular cloning of the gene for a conserved major immunoreactive			
RT	28-kilodalton protein of Ehrlichia canis: a potential serodiagnostic			
RT	antigen.";			
RL	Clin. Diagn. Lab. Immunol. 6:392-399(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Jake;			
RX	MEDLINE=20432107; PubMed=10974556; DOI=10.1016/S0378-1119(00)00256-0;			
RA	McBride J.W., Yu X.J., Walker D.H.;			
RT	"A conserved, transcriptionally active p28 multigene locus of			
RT	Ehrlichia canis.";			
RL	Gene 254:245-252(2000).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=OklaHoma;			
RX	MEDLINE=98371112; PubMed=9705412;			
RA	Obashi N., Unver A., Zhi N., Rikhsa Y.;			
RT	"Cloning and characterization of multigenes encoding the			
RT	immunodominant 30-kilodalton major outer membrane proteins of			
RT	Ehrlichia canis and application of the recombinant protein for			
RT	serodiagnosis.";			
RL	J. Clin. Microbiol. 36:2671-2680(1998).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=OklaHoma;			
RX	MEDLINE=21153566; PubMed=11254561;			
RA	DOI=10.1128/IAI.69.4.2083-2091.2001;			
RT	Obashi N., Rikhsa Y., Unver A.;			
RT	"Analysis of transcriptionally active gene clusters of major outer			
RT	membrane protein multigene family in Ehrlichia canis and E.			
RT	chaffeensis.";			
RL	Infect. Immun. 69:2083-2091(2001).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Arizona, California, New Mexico, and Venezuela;			
RX	MEDLINE=22461952; PubMed=12574308;			

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OM nucleic - nucleic search, using SW model

Run on: February 19, 2005, 20:16:34 ; Search time 623 Seconds  
(without alignments)  
7969.209 Million cell updates/sec

File: US-10-680-349-41

Perfect score: 840  
Sequence: 1 atgaatcataagaataatctt.....cttgatgaggttcaccttc 840

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 5384158 seqs, 2955248155 residues

Total number of hits satisfying chosen parameters: 10768316

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*
- 14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/2/pubpna/US10D\_PUBCOMB.seq:\*
- 17: /cgn2\_6/ptodata/2/pubpna/US10E\_PUBCOMB.seq:\*
- 18: /cgn2\_6/ptodata/2/pubpna/US10F\_PUBCOMB.seq:\*
- 19: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*
- 20: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUBCOMB.seq:\*
- 21: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 22: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	840	100.0	840	10	US-09-811-007-41 Sequence 41, Appl
2	840	100.0	840	13	US-10-062-624-41 Sequence 41, Appl
3	840	100.0	840	14	US-10-062-051-41 Sequence 41, Appl
4	840	100.0	840	14	US-10-062-920-41 Sequence 41, Appl
5	840	100.0	840	18	US-10-680-349-41 Sequence 41, Appl
6	840	100.0	840	18	US-10-731-554-41 Sequence 41, Appl
7	840	100.0	843	13	US-10-059-964-47 Sequence 47, Appl
8	840	100.0	843	15	US-10-314-639-35 Sequence 35, Appl
9	840	100.0	843	18	US-10-901-714-35 Sequence 35, Appl
10	840	100.0	843	18	US-10-901-714-47 Sequence 47, Appl
11	598.6	71.3	852	13	US-10-059-964-3 Sequence 3, Appl

12	598.6	71.3	852	15	US-10-314-639-3 Sequence 3, Appl
13	598.6	71.3	852	18	US-10-901-714-3 Sequence 3, Appl
14	598.6	71.3	852	18	US-10-901-714-3 Sequence 3, Appl
15	238.4	28.4	924	13	US-10-059-964-35 Sequence 35, Appl
16	238.4	28.4	924	15	US-10-314-639-35 Sequence 35, Appl
17	238.4	28.4	924	18	US-10-901-714-35 Sequence 35, Appl
18	238.4	28.4	924	18	US-10-901-714-35 Sequence 35, Appl
19	238.4	28.4	1607	10	US-09-811-007-1 Sequence 1, Appl
20	238.4	28.4	1607	13	US-10-062-624-1 Sequence 1, Appl
21	238.4	28.4	1607	14	US-10-062-051-1 Sequence 1, Appl
22	238.4	28.4	1607	14	US-10-062-920-1 Sequence 1, Appl
23	238.4	28.4	1607	18	US-10-680-349-1 Sequence 1, Appl
24	238.4	28.4	1607	18	US-10-731-554-1 Sequence 1, Appl
25	234	27.9	840	10	US-09-811-007-5 Sequence 5, Appl
26	234	27.9	840	13	US-10-062-624-5 Sequence 5, Appl
27	234	27.9	840	14	US-10-062-051-5 Sequence 5, Appl
28	234	27.9	840	14	US-10-062-920-5 Sequence 5, Appl
29	234	27.9	840	18	US-10-680-349-5 Sequence 5, Appl
30	234	27.9	840	18	US-10-731-554-5 Sequence 5, Appl
31	234	27.9	846	18	US-10-901-714-1 Sequence 1, Appl
32	234	27.9	846	18	US-10-901-714-1 Sequence 1, Appl
33	232.4	27.7	843	13	US-10-059-964-37 Sequence 37, Appl
34	232.4	27.7	843	15	US-10-314-639-37 Sequence 37, Appl
35	232.4	27.7	843	18	US-10-901-714-37 Sequence 37, Appl
36	232.4	27.7	843	18	US-10-901-714-37 Sequence 37, Appl
37	232.4	27.7	846	13	US-10-059-964-1 Sequence 1, Appl
38	232.4	27.7	846	15	US-10-314-639-1 Sequence 1, Appl
39	228.6	27.2	830	13	US-10-062-994-11 Sequence 11, Appl
40	228.6	27.2	830	18	US-10-722-077-11 Sequence 11, Appl
41	217.4	25.9	867	13	US-10-059-964-31 Sequence 31, Appl
42	217.4	25.9	867	15	US-10-314-639-31 Sequence 31, Appl
43	217.4	25.9	867	18	US-10-901-714-31 Sequence 31, Appl
44	217.4	25.9	867	18	US-10-901-714-31 Sequence 31, Appl
45	217.4	25.9	867	18	US-10-901-714-31 Sequence 31, Appl

#### ALIGNMENTS

RESULT 1  
US-09-811-007-41  
Sequence 41, Application US/09811007  
Publication No. US20030185849A1  
GENERAL INFORMATION:  
APPLICANT: Walker, David H.  
APPLICANT: McBride, Jere W.  
TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein  
FILE REFERENCE: D6152CIP2  
CURRENT APPLICATION NUMBER: US/09/811,007  
CURRENT FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 09/660,587  
PRIOR FILING DATE: 2000-09-12  
NUMBER OF SEQ ID NOS: 46  
SEQ ID NO 41  
LENGTH: 840  
TYPE: DNA  
ORGANISM: *Ehrlichia canis*  
FEATURE:  
OTHER INFORMATION: nucleic acid sequence of *E. canis* p28-2  
US-09-811-007-41

Query Match 100.0%; Score 840; DB 10; Length 840;  
Best Local Similarity 100.0%; Pred. No. 5.5e-172;  
Matches 840; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATTAATAGAAATTTAGTAAGAGCGCTTATCTCATTTATGTCATCTTACCA 60  
DB 1 ATGAATTAATAGAAATTTAGTAAGAGCGCTTATCTCATTTATGTCATCTTACCA 60  
QY 61 TATCACTTTTTCGACATCTCTAGGTTCAAGACTTAATGATTAACAAGAGCTTCTAC 120



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OM nucleic - nucleic search, using sw model

Run on: February 19, 2005, 15:10:13 ; Search time 589 Seconds

(without alignment)  
8442.415 Million cell updates/sec

Title: US-10-680-349-41

Perfect score: 840  
Sequence: 1 atgaattactagaagaattctt.....ttggaatgaggttcaccttc 840

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

N\_Geneseq\_16Dec04:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001bs:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	840	100.0	840	6	ABK68876
2	840	100.0	843	6	ABK68876
3	840	100.0	843	9	ABK68876
4	600.2	71.5	852	2	AAK34744
5	600.2	71.5	852	6	ABK68876
6	598.6	71.3	852	9	ABK68876
7	450.8	53.7	849	2	AAK34744
8	450.8	53.7	849	6	ABK68876
9	238.4	28.4	924	2	AAK34744
10	238.4	28.4	924	6	ABK68876
11	238.4	28.4	924	9	ABK68876
12	238.4	28.4	1607	3	ABK68876
13	238.4	28.4	1607	6	ABK68876
14	238.4	28.4	1607	9	ABK68876
15	234	27.9	840	6	ABK68876
16	234	27.9	840	9	ABK68876
17	234	27.9	846	6	ABK68876
18	234	27.9	2037	3	AAK34744
19	232.4	27.7	843	2	AAK34744
20	232.4	27.7	843	6	ABK68876

21	232.4	27.7	843	9	ADA09770	ADA09770 E. canis
22	232.4	27.7	846	2	AAK34743	AAK34743 DNA encod
23	232.4	27.7	846	9	ADA09734	ADA09734 E. chaffe
24	228.6	27.2	830	3	AAK68706	AAK68706 Ehrlichia
25	228.6	27.2	4683	3	AAV07179	AAV07179 Ehrlichia
26	228.6	27.2	4683	3	AAK68716	AAK68716 Ehrlichia
27	228.6	27.2	4683	4	AAK07578	AAK07578 DNA encod
28	217.4	25.9	867	2	AAK34759	AAK34759 DNA encod
29	217.4	25.9	867	6	ABK63291	ABK63291 DNA encod
30	217.4	25.9	867	9	ADA09764	ADA09764 E. canis
31	212.8	25.3	861	2	AAK34746	AAK34746 DNA encod
32	212.8	25.3	861	3	AAK68703	AAK68703 Ehrlichia
33	212.8	25.3	861	6	ABK63279	ABK63279 DNA encod
34	212.8	25.3	861	9	ADA09740	ADA09740 E. chaffe
35	210.4	25.0	756	6	ABK63307	ABK63307 Ehrlichia
36	208.8	24.9	756	6	AAK34742	AAK34742 DNA encod
37	207.2	24.7	843	2	AAK34748	AAK34748 DNA encod
38	207.2	24.7	843	3	AAK68705	AAK68705 Ehrlichia
39	207.2	24.7	843	6	ABK63281	ABK63281 DNA encod
40	207.2	24.7	843	9	ADA09744	ADA09744 E. chaffe
41	205	24.4	837	2	AAK34747	AAK34747 DNA encod
42	205	24.4	837	3	AAK68704	AAK68704 Ehrlichia
43	205	24.4	837	6	ABK63280	ABK63280 DNA encod
44	205	24.4	837	9	ADA09742	ADA09742 E. chaffe
45	203.8	24.3	842	2	AAV07177	AAV07177 Ehrlichia

## ALIGNMENTS

RESULT 1	ABK68876	standard; DNA; 840 BP.
ID	ABK68876	
XX	ABK68876	
AC	ABK68876	
XX		
DT	02-JUL-2002	(first entry)
XX		
DE	DNA encoding Ehrlichia canis p28-2.	
XX		
KW	Ehrlichia canis infection; vaccine; serodiagnostic; gene; p28; ss;	
XX	antibacterial.	
OS	Ehrlichia canis.	
XX		
PN	WO200222782-A2.	
XX		
PD	21-MAR-2002.	
XX		
PF	12-SEP-2001; 2001WO-US028759.	
XX		
PR	12-SEP-2000; 2000US-00660587.	
XX		
PA	(RERE-) RES DEV FOUND.	
XX		
PI	Walker DH, Yu X, McBride JW;	
XX		
DR	WPI; 2002-351882/38.	
XX		
PT	P-PSDB; AAU96116.	
XX		
PT	New recombinant homologous 28 kilodalton immunodominant protein from	
XX	Ehrlichia canis, useful for treating Ehrlichia canis infections.	
PS	Claim 5; Fig 14; 106pp; English.	
XX		
CC	The invention relates to a recombinant homologous 28 kDa immunodominant	
CC	protein, p28 (I) of Ehrlichia canis. (I), a 28-kDa antigen preferably	
CC	dispersed in a pharmaceutically acceptable carrier, is useful for	
CC	inhibiting E. canis infection in a subject. (I) is useful in the	
CC	development of vaccines and serodiagnostic that are particularly	
CC	effective for disease prevention and serodiagnosis. ABK68876	
CC	represent the 28-kDa antigen coding sequences and PCR primers of the	
CC	invention	

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using BW model

Run on: February 19, 2005, 18:42:08 ; Search time 194 Seconds  
(without alignments)  
7084.910 Million cell updates/sec

Title: US-10-680-349-41

Perfect score: 840  
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Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

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Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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3	840	100.0	843	4	US-09-314-701-47
4	598.6	71.3	852	4	US-09-314-701-3
5	243.4	29.0	849	3	US-09-648-520E-48
6	238.4	28.4	924	4	US-09-314-701-35
7	238.4	28.4	1607	3	US-09-660-587-1
8	238.4	28.4	1607	3	US-09-261-358A-1
9	238.4	28.4	1607	3	US-09-648-520E-47
10	238.4	28.4	1607	3	US-09-201-458-1
11	238.4	28.4	1607	4	US-09-811-007A-1
12	234	27.9	840	3	US-09-660-587-5
13	234	27.9	840	3	US-09-261-358A-5
14	234	27.9	840	3	US-09-811-007A-5
15	232.4	27.7	846	4	US-09-314-701-37
16	232.4	27.7	846	4	US-09-314-701-1
17	228.6	27.2	830	3	US-08-953-326-11
18	228.6	27.2	830	3	US-09-553-662-11
19	228.6	27.2	830	4	US-10-062-994-11
20	217.4	25.9	867	4	US-09-314-701-31
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22	212.8	25.3	861	4	US-09-314-701-7
23	212.8	25.3	861	4	US-09-553-662-8
24	212.8	25.3	861	4	US-10-062-994-8
25	207.2	24.7	843	3	US-08-953-326-10
26	207.2	24.7	843	4	US-09-314-701-11
27	207.2	24.7	843	4	US-09-553-662-10

28	207.2	24.7	843	4	US-10-062-994-10	Sequence 10, Appl
29	205	24.4	837	3	US-08-953-326-9	Sequence 9, Appl
30	205	24.4	837	4	US-09-314-701-9	Sequence 9, Appl
31	205	24.4	837	4	US-09-553-662-9	Sequence 9, Appl
32	205	24.4	837	4	US-10-062-994-9	Sequence 9, Appl
33	203.8	24.3	842	3	US-08-733-230-3	Sequence 3, Appl
34	203.8	24.3	842	3	US-08-953-326-3	Sequence 3, Appl
35	203.8	24.3	842	4	US-09-553-662-3	Sequence 3, Appl
36	203.8	24.3	842	4	US-10-062-994-3	Sequence 3, Appl
37	198.4	23.6	843	4	US-09-314-701-5	Sequence 5, Appl
38	195	23.2	828	3	US-09-660-587-43	Sequence 43, Appl
39	195	23.2	828	4	US-09-811-007A-43	Sequence 43, Appl
40	195	23.2	864	3	US-08-733-230-1	Sequence 1, Appl
41	195	23.2	864	3	US-08-953-326-1	Sequence 1, Appl
42	195	23.2	864	4	US-09-553-662-1	Sequence 1, Appl
43	195	23.2	864	4	US-10-062-994-1	Sequence 1, Appl
44	191.8	22.8	831	4	US-09-314-701-41	Sequence 41, Appl
45	185.4	22.1	840	4	US-09-314-701-23	Sequence 23, Appl

## ALIGNMENTS

```
RESULT 1
US-09-660-587-41
; Sequence 41, Application US/09660587
; Patent No. 6392023
; GENERAL INFORMATION:
; APPLICANT: Walker, David H.
; APPLICANT: McBride, Jere W.
; APPLICANT: Yu, Xue-Yie
; TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein
; FILE REFERENCE: D6152CP2
; CURRENT APPLICATION NUMBER: US/09/660,587
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 09/261,358
; PRIOR FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 46
; SEQ ID NO 41
; LENGTH: 840
; TYPE: DNA
; ORGANISM: Ehrlichia canis
; FEATURE:
; OTHER INFORMATION: nucleic acid sequence of E. canis p28-2
US-09-660-587-41

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Best Local Similarity 100.0%; Pred. No. 1.1e-211;
Matches 840; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      181 CCAATTATAGAACAAATTCCTCACAAAGTTTCCGACCTAAAGAAAGTGGAT 240
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QY      241 ATTAACAAAAAGAGATTTTACAGAGTACTCCAGCATTTTCAAAATTACTTA 300
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OM nucleic - nucleic search, using sw model

Run on: February 19, 2005, 18:37:19 ; Search time 3559 Seconds  
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8983.980 Million cell updates/sec

Title: US-10-680-349-41

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Gapop 10.0, Gapexc 1.0

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Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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4: gb\_est3.\*  
5: gb\_est4.\*  
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7: gb\_est6.\*  
8: gb\_gsa1.\*  
9: gb\_gsa2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	68.6	8.2	1101	9	CNS00EVL
2	63.4	7.5	750	9	AL100303 Drosophila
3	59.2	7.0	895	8	AZ550258 ENTFU14TF
4	58.2	6.9	875	8	AZ550139 ENTFU47TR
5	56.8	6.8	927	8	AZ549936 ENTFE86TR
6	56.8	6.8	937	8	BH155225 ENTFH30TR
7	55.8	6.6	889	8	AZ547516 ENTFM38TF
8	55.8	6.6	1101	9	CNS0039G
9	55	6.5	627	5	BQ475055 carabua3
10	55	6.5	770	5	BQ474983 carabua3
11	55	6.5	1101	9	CNS0039G
12	54.8	6.5	1348	9	CG749499 P043-4-A0
13	54.2	6.5	639	9	CNS0170D
14	54.2	6.5	939	8	BH133767 ENTFU23TF
15	53.6	6.4	897	8	AZ551013 ENTFU54TR
16	53	6.3	1101	9	CNS0176
17	52.8	6.3	895	8	BH163498 ENTFQ70TR
18	52.8	6.3	922	8	BH136172 ENTFX40TF
19	52.4	6.2	984	9	CL113045 ISB1-57P1
20	52.4	6.2	1487	9	ACG390845 Mus muscu
21	52	6.2	841	8	AZ689408 ENTFX95TR
22	51.8	6.2	884	8	CNS0129A
23	51.6	6.1	606	4	B1441163
24	51.6	6.1	819	8	AZ677439 ENTFI69TR

C 25	51.6	6.1	833	8	AZ544101	AZ544101 ENTFP80TF
C 26	51.6	6.1	912	8	AZ545164	AZ545164 ENTFW83TR
C 27	51.6	6.1	912	8	BH158221	ENTSD60TF
C 28	51.6	6.1	917	8	BH166533	ENTSV42TF
C 29	51.6	6.1	928	8	BH164168	ENTSZ24TR
C 30	51.4	6.1	878	8	CNS0187R	Drosophila
C 31	51.2	6.1	884	8	AZ689586	ENTHU07TR
C 32	51	6.1	898	8	AZ538693	AZ538693 ENTF573TF
C 33	51	6.1	932	8	BH132524	ENTNE36TF
C 34	50.8	6.0	1001	9	CNS0155H	AL105023 Drosophila
C 35	50.6	6.0	747	9	CNS011RO	AL100640 Drosophila
C 36	50.6	6.0	1013	9	AG564361	AG564361 Mus muscu
C 37	50.6	6.0	1224	9	AG305050	AG305050 Mus muscu
C 38	50.4	6.0	649	4	BH160056	BH160056 EST562579
C 39	50.4	6.0	852	8	AZ529741	ENTCA60TR
C 40	50.2	6.0	1201	9	AG390499	Mus muscu
C 41	50	6.0	481	4	B1333673	k166a05.Y
C 42	50	6.0	762	4	AG524600	Mus muscu
C 43	50	6.0	885	8	BH167558	ENTRZ50TR
C 44	50	6.0	886	8	BH146655	ENTPE52TF
C 45	50	6.0	908	8	BH152307	ENTPV06TR

#### ALIGNMENTS

RESULT 1  
CNS00EVL 1101 bp DNA linear GSS 04-JUN-1999  
LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC:  
DEFINITION BACR29B23 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION AL069706.1 GI:4949849

VERSION AL069706

KEYWORDS GSS.

SOURCE Drosophila melanogaster (fruit fly)

ORGANISM Drosophila melanogaster

REFERENCE 1 (bases 1 to 1101)

AUTHORS Genoscope.

TITLE Direct Submission

JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr)

COMMENT - Web : www.genoscope.cns.fr

Determination of this BAC-end sequence was carried out as part of a

collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila

melanogaster genome using these BACs. For further information

please see <http://www.fruitfly.org> The BDGP Drosophila

melanogaster BAC library was prepared by Kazuo Osega and

Aaron Mammone in Peter de Jong's laboratory in the Department of

Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,

NY. The library is named RPCI-98 and was constructed by partial

ecori digestion of Drosophila DNA provided by the BDGP from the

isogenic strain y2; cn bw sp, the same strain used for the BDGP's

pl and EST libraries. A more detailed description of the library

and how to order individual BAC clones, the entire library, or

filters for hybridization from the BACAC Resource Center can be

found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

#### FEATURES

source

1. 1101

/organism="Drosophila melanogaster"

/mol\_type="genomic DNA"

/db\_xref="taxon:7227"

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/clone\_lib="RPCI-98"

/note="end : T7"

#### ORIGIN

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Best local similarity 34.7%; Pred. NO. 1.5e-05;

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 19, 2005, 17:06:08 ; Search time 4113 Seconds  
(without alignments)  
9896.032 Million cell updates/sec

Title: US-10-680-349-41

Perfect score: 840  
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Gapop 10.0, Gapext 1.0

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Maximum DB seq length: 2000000000

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Maximum Match 100%  
Listing first 45 summaries

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12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match length	ID	Description
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2	840	100.0	843 6	AR303107 Sequence
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4	840	100.0	906 1	AF528512 Ehrlichia
5	840	100.0	906 1	AF528514 Ehrlichia
6	840	100.0	906 1	AF528515 Ehrlichia
7	840	100.0	6913 1	AF324792 Ehrlichia
8	840	100.0	11329 1	AF082744 Ehrlichia
9	840	100.0	28254 1	AF078553 Ehrlichia
10	835.2	99.4	906 1	AF528513 Ehrlichia
11	616.2	73.4	5828 1	AF479838 Ehrlichia
12	616.2	73.4	5857 1	AF479835 Ehrlichia
13	616.2	73.4	5857 1	AF479836 Ehrlichia
14	613	73.0	5857 1	AF479837 Ehrlichia
15	606.6	72.2	6941 1	AF479840 Ehrlichia
16	606.6	72.2	6954 1	AF479839 Ehrlichia
17	600.2	71.5	7041 1	AF479833 Ehrlichia
18	600.2	71.5	7049 1	AF479834 Ehrlichia
19	600.2	71.5	27190 1	ECU72291 Ehrlichia c

20	598.6	71.3	852 6	AR303085 Sequence
21	528.2	62.9	3507 1	AF125276 Cowdria r
22	528.2	62.9	3535 1	AF125274 Cowdria r
23	528.2	62.9	3538 1	AF125277 Cowdria r
24	528.2	62.9	3541 1	AF125279 Cowdria r
25	528.2	62.9	3551 1	AF125275 Cowdria r
26	528.2	62.9	3572 1	AF125278 Cowdria r
27	528.2	62.9	24992 1	AY343331 Ehrlichia
28	457.6	54.5	2362 1	AF319940 Cowdria r
29	238.4	28.4	834 1	AF082745 Ehrlichia
30	238.4	28.4	834 1	AF082746 Ehrlichia
31	238.4	28.4	834 1	AF082747 Ehrlichia
32	238.4	28.4	834 1	AF082748 Ehrlichia
33	238.4	28.4	834 1	AF082749 Ehrlichia
34	238.4	28.4	834 1	AF082750 Ehrlichia
35	238.4	28.4	924 6	AR303101 Sequence
36	238.4	28.4	1607 6	AR213516 Sequence
37	238.4	28.4	1607 6	AR235244 Sequence
38	238.4	28.4	1607 6	AR437310 Sequence
39	234	27.9	840 6	AR213518 Sequence
40	234	27.9	840 6	AR437312 Sequence
41	234	27.9	1050 1	AY117396 Ehrlichia
42	234	27.9	1342 1	AF393388 Ehrlichia
43	233.2	27.8	1315 1	AF393392 Ehrlichia
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#### ALIGNMENTS

RESULT 1  
AR437334  
LOCUS AR437334  
DEFINITION Sequence 41 from patent US 660269.  
ACCESSION AR437334  
VERSION AR437334.1 GI:40202246  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 840)  
AUTHORS Walker, D.H., Yu, X.-J. and McBride, J.W.  
TITLE Homologous 28-kilodalton immunodominant protein genes of Ehrlichia  
cantis and uses thereof  
JOURNAL Patent: US 660269-A 41 09-DEC-2003;  
FEATURES  
source Location/Qualifiers  
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/mol\_type="genomic DNA"

#### ORIGIN

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Best Local Similarity 100.0%; Pred. No. 3, 1e-140;  
Matches 840; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGAATTATAGAAATTTCTAGTAAAGCGCTTAATCTTAAATGTCATCTTACCA 60  
DB 1 ATGAATTATAGAAATTTCTAGTAAAGCGCTTAAATCTTAAATGTCATCTTACCA 60  
QY 61 TATCAGCTTTTGCAAGTCTCTGTTCAAGAACTAATGATACCAAGAGCTTCTAC 120  
DB 61 TATCAGCTTTTGCAAGTCTCTGTTCAAGAACTAATGATACCAAGAGCTTCTAC 120  
QY 121 ATTGTCGAAGTCAATCAAGTATATCACTTTAGAAATTTCTGCTGAGAAACT 180  
DB 121 ATTGTCGAAGTCAATCAAGTATATCACTTTAGAAATTTCTGCTGAGAAACT 180  
QY 181 CCTATTATGGAACAATTTCTTCACTTAAAGTTTTCGACTTAAAGAAAGATGGTAT 240  
DB 181 CCTATTATGGAACAATTTCTTCACTTAAAGTTTTCGACTTAAAGAAAGATGGTAT 240  
QY 241 ATAACAAAAAGACGATTTTACAGAGTGCACGACATGATTTTCAAAATACCTA 300

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 DB 1 MNYKKILVRSALISLMSILPYOSPADVSGRTDNKEGFIYISAKYNPSISHFRKFSAEET 60  
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 DB 61 PINGNSLTGKVFGLKKGDDITKKDPTFRVAPGIDPQNNLISGFSGSIYSGMDGPRIELE 120  
 QY 121 AAYQFNPKNNTDNDTNGEYRKHFPALSRKDAMEDOQYVVLKNDGITPMSLMVNTCYDIT 180  
 DB 121 AAYQFNPKNNTDNDTNGEYRKHFPALSRKDAMEDOQYVVLKNDGITPMSLMVNTCYDIT 180  
 QY 181 AEGVSFVPYACAGIGADLITTFKDLNLKFAVOGKIGISYPTPEVSATFGYHYGVGNK 240  
 DB 181 AEGVSFVPYACAGIGADLITTFKDLNLKFAVOGKIGISYPTPEVSATFGYHYGVGNK 240  
 QY 241 FEKIPVITPVVNDAPQTSASVTLDVGYFGSEIGRFTF 280  
 DB 241 FEKIPVITPVVNDAPQTSASVTLDVGYFGSEIGRFTF 280

## RESULT 2

ABG77958  
 ID ABG77958 standard; protein; 280 AA.

AC ABG77958;

DT 15-NOV-2002 (first entry)

DE Ehrlichia canis outer membrane protein (P30F) #9.

KW Outer membrane protein; OMP; P30F; ehrlichiosis; infection.

OS Ehrlichia canis.

PN US2002120115-A1.

PD 29-AUG-2002.

PF 28-JAN-2002; 2002US-00059964.

PR 19-MAY-1999; 99US-00314701.

PA (RIKI/) RIKIHISA Y.

PI (OHAS/) OHASHI N.

PI Rikihisa Y, Ohashi N;

WPI; 2002-618954/66.

DR N-PSDB; ABS63299.

PT Isolated polynucleotide encoding an outer membrane protein of E. canis or

PS Claim 10; Fig 30B; 49pp; English.

CC The invention relates to an isolated polynucleotide encoding an outer  
 CC membrane protein (OMP) of Ehrlichia canis or Ehrlichia chaffeensis used  
 CC in the diagnosis of infection. An infection such as human ehrlichiosis or  
 CC canine ehrlichiosis can be diagnosed by providing a serum sample from the  
 CC patient, providing a polypeptide or mixture of polypeptides, contacting  
 CC the sample with the polypeptide and assaying for the formation of a  
 CC complex between antibodies in the serum sample and the polypeptide, where  
 CC formation of a complex is indicative of infection with E. chaffeensis.  
 CC This sequence represents an Ehrlichia outer membrane protein of the  
 CC invention

SO Sequence 280 AA;

Query Match 100.0%; Score 1462; DB 5; Length 280;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-138;  
 Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNYKKILVRSALISLMSILPYOSPADVSGRTDNKEGFIYISAKYNPSISHFRKFSAEET 60  
 DB 1 MNYKKILVRSALISLMSILPYOSPADVSGRTDNKEGFIYISAKYNPSISHFRKFSAEET 60  
 QY 61 PINGNSLTGKVFGLKKGDDITKKDPTFRVAPGIDPQNNLISGFSGSIYSGMDGPRIELE 120  
 DB 61 PINGNSLTGKVFGLKKGDDITKKDPTFRVAPGIDPQNNLISGFSGSIYSGMDGPRIELE 120  
 QY 121 AAYQFNPKNNTDNDTNGEYRKHFPALSRKDAMEDOQYVVLKNDGITPMSLMVNTCYDIT 180  
 DB 121 AAYQFNPKNNTDNDTNGEYRKHFPALSRKDAMEDOQYVVLKNDGITPMSLMVNTCYDIT 180  
 QY 181 AEGVSFVPYACAGIGADLITTFKDLNLKFAVOGKIGISYPTPEVSATFGYHYGVGNK 240  
 DB 181 AEGVSFVPYACAGIGADLITTFKDLNLKFAVOGKIGISYPTPEVSATFGYHYGVGNK 240  
 QY 241 FEKIPVITPVVNDAPQTSASVTLDVGYFGSEIGRFTF 280  
 DB 241 FEKIPVITPVVNDAPQTSASVTLDVGYFGSEIGRFTF 280

## RESULT 3

ADA09781  
 ID ADA09781 standard; protein; 280 AA.

AC ADA09781;

DT 06-NOV-2003 (first entry)

DE E. canis outer membrane protein P30-10.

KW outer membrane protein; circulating leukocyte; monocyte ehrlichiosis;  
 KW Rocky Mountain spotted fever; canine ehrlichiosis; antigen.

OS Ehrlichia canis.

PN US6544517-B1.

PD 08-APR-2003.

PF 19-MAY-1999; 99US-00314701.

PR 18-SEP-1998; 98US-0100843P.

PA (OHIS ) UNIV OHIO STATE RES FOUND.

PI Rikihisa Y, Ohashi N;

WPI; 2003-553952/52.

DR N-PSDB; ADA09780.

PT New isolated polynucleotide encoding outer membrane protein p30 of  
 PT Ehrlichia canis or its variant or fragment, useful for producing  
 PT Ehrlichia canis or Ehrlichia chaffeensis outer membrane proteins for  
 PT diagnosing and treating ehrlichiosis.

PS Disclosure, Fig 30; 105pp; English.

CC The invention relates to an isolated polynucleotide encoding a variant of  
 CC the outer membrane protein (OMP) P30 of Ehrlichia canis, an outer  
 CC membrane protein of E. canis, or an antigenic fragment of the E. canis  
 CC P30 protein, or comprising a sequence which is the complement of  
 CC nucleotide 99 through nucleotide 672 of ADA09764. Also disclosed are E.  
 CC canis and E. chaffeensis outer membrane proteins and their encoding  
 CC nucleic acids. The polynucleotides are useful for producing E. canis or  
 CC E. chaffeensis outer membrane protein, for designing hybridisation probes  
 CC or its allelic forms, for designing primers for PCR. The polypeptides  
 CC encoded by the polynucleotide is useful for diagnosing human ehrlichiosis  
 CC (Rocky mountain spotted fever) or canine ehrlichiosis. The present  
 CC sequence represents an E. canis outer membrane protein.

SO Sequence 280 AA;

Query Match 100.0%; Score 1462; DB 6; Length 280;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-138;  
 Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MNYKILVRSALISLMSILPYOSFADPVGSRTDNKEGYISAKNPSISHRKPSAERT 60
DB 1 MNYKILVRSALISLMSILPYOSFADPVGSRTDNKEGYISAKNPSISHRKPSAERT 60
QY 61 PINGNSLTKKVFGLKKGDDITKODFTVAPEIDFQNNLISGFSGISYMDGPRIE 120
DB 61 PINGNSLTKKVFGLKKGDDITKODFTVAPEIDFQNNLISGFSGISYMDGPRIE 120
QY 121 AAQGFNPKNNTDNDTNGEYKHFALSRKDMEDQYVVLKNDGTFMSLWNTCYDT 180
DB 121 AAQGFNPKNNTDNDTNGEYKHFALSRKDMEDQYVVLKNDGTFMSLWNTCYDT 180
QY 181 AAGVSVFPYACAGIGADLITTFKDLMLKFAVGKIGISYPTPEVSAPFGYHGVIG 240
DB 181 AAGVSVFPYACAGIGADLITTFKDLMLKFAVGKIGISYPTPEVSAPFGYHGVIG 240
QY 241 FEKIPVITPVVNDAPQTTSASVTLDVGFGEIGMRTF 280
DB 241 FEKIPVITPVVNDAPQTTSASVTLDVGFGEIGMRTF 280

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## RESULT 4

ID AA06944 standard; protein; 283 AA.

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XX AC AA06944;
XX DT 27-AUG-2003 (revised)
XX DT 05-JUL-1999 (first entry)
XX DE E. chaffeensis OMP-1B protein.
XX KW Outer membrane protein; OMP; Ehrlichia chaffeensis; E. canis; P30;
XX KW detection; dog.
XX OS Ehrlichia chaffeensis.
XX PN W09913720-A1.
XX PD 25-MAR-1999.
XX PF 18-SEP-1998; 98WO-US019600.
XX PR 19-SEP-1997; 97US-0059353P.
XX PA (OHIS ) UNIV OHIO STATE.
XX PI Rikihia Y, Ohashi N;
XX PT WPI; 1999-254290/21.
XX DR N-PSDB; AA034744.
XX PT Novel outer membrane proteins from Ehrlichia chaffeensis and Ehrlichia
XX PT canis.
XX PS Claim 12; Fig 4B; 55pp; English.
XX CC The invention provides isolated outer membrane proteins (OMP) from
XX CC Ehrlichia chaffeensis and E. canis. The E. chaffeensis proteins form part
XX CC of the OMP family and consist of proteins OMP-1, -1(B to Z) shown in
XX CC AA06943-958. The E. canis proteins form part of the P30 family and
XX CC consist of proteins shown in AA06959-970. The proteins and genes are
XX CC used to detect E. chaffeensis in patients and E. canis in dogs. (Updated
XX CC on 27-AUG-2003 to correct OS field.)
XX SQ Sequence 283 AA;

```

Query Match 82.3%; Score 1202.5; DB 2; Length 283;

Best Local Similarity 79.5%; Pred. No. 2.6e-112;  
 Matches 225; Conservative 26; Mismatches 29; Indels 3; Gaps 1;

```

QY 1 MNYKILVRSALISLMSILPYOSFADPVGSRTDNKEGYISAKNPSISHRKPSA 57
DB 1 MNYKILVRSALISLMSILPYOSFADPVGSRTDNKEGYISAKNPSISHRKPSA 60
QY 58 EETPINGNSLTKKVFGLKKGDDITKODFTVAPEIDFQNNLISGFSGISYMDGPRI 117
DB 61 EETPINGNSLTKKVFGLKKGDDITKODFTVAPEIDFQNNLISGFSGISYMDGPRI 120
QY 118 EIEAAVQGFNPKNNTDNDTNGEYKHFALSRKDMEDQYVVLKNDGTFMSLWNTCY 177
DB 121 EIEAAVQGFNPKNNTDNDTNGEYKHFALSRKDMEDQYVVLKNDGTFMSLWNTCY 180
QY 178 DITAGSVFPYACAGIGADLITTFKDLMLKFAVGKIGISYPTPEVSAPFGYHGV 237
DB 181 DITAGSVFPYACAGIGADLITTFKDLMLKFAVGKIGISYPTPEVSAPFGYHGV 240
QY 238 GNFPEKIPVITPVVNDAPQTTSASVTLDVGFGEIGMRTF 280
DB 241 GNFPEKIPVITPVVNDAPQTTSASVTLDVGFGEIGMRTF 283

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## RESULT 5

ID AA06106 standard; protein; 283 AA.

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XX AC AA06106;
XX DT 07-AUG-2003 (revised)
XX DT 02-JUL-2002 (first entry)
XX DE Ehrlichia chaffeensis OMP-1B.
XX KW Ehrlichia canis infection; vaccine; serodiagnostic; p28; antibacterial.
XX KW Ehrlichia chaffeensis.
XX OS Ehrlichia chaffeensis.
XX PN W0200222782-A2.
XX PD 21-MAR-2002.
XX PF 12-SEP-2001; 2001WO-US028759.
XX PR 12-SEP-2000; 2000US-00660587.
XX PA (RERE-) RES DEV FOUND.
XX PI Walker DH, Yu X, McBride JW;
XX PT WPI; 2002-351882/38.
XX PT New recombinant homologous 28 kilodalton immunodominant protein from
XX PT Ehrlichia canis, useful for treating Ehrlichia canis infections.
XX PS Example 3; Fig 3; 106pp; English.
XX CC The invention relates to a recombinant homologous 28 kDa immunodominant
XX CC protein, p28, (I), of Ehrlichia canis. (I), a 28-kDa antigen preferably
XX CC dispersed in a pharmaceutically acceptable carrier, is useful for
XX CC inhibiting E. canis infection in a subject. (I) is useful in the
XX CC development of vaccines and serodiagnostic tests that are particularly
XX CC effective for disease prevention and serodiagnosis. AA06100-AA06118
XX CC represent the 28-kDa antigen amino acid sequences of the invention.
XX CC (Updated on 07-AUG-2003 to correct OS field.)
XX SQ Sequence 283 AA;

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Query Match 82.3%; Score 1202.5; DB 5; Length 283;  
 Best Local Similarity 79.5%; Pred. No. 2.6e-112;  
 Matches 225; Conservative 26; Mismatches 29; Indels 3; Gaps 1;